Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: 08/944544

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 ____ Wrong Designation
Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source f genetic material in <220> t <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

J. Reeves

> **This Raw Listing contains the General Information
> Section and up to first 5 pages.**

Does Not Comply
Corrected Diskette Needed

```
 1   <110> APPLICANT: SADELAIN, MICHEL
 2          CHEUNG, NAI-KONG V.
 3          KRAUSE, ANJA
 4          GUO, HONG-FEN
 5   <120> TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND
 6          USES THEREOF
 7   <130> FILE REFERENCE: MSK.P-035-US
 8   <140> CURRENT APPLICATION NUMBER: US/08/940,544
 9   <141> CURRENT FILING DATE: 1997-09-30
10   <150> EARLIER APPLICATION NUMBER: PCT/US97/04427
11   <151> EARLIER FILING DATE: 1997-03-20
12   <160> NUMBER OF SEQ ID NOS: 4
13   <170> SOFTWARE: PatentIn Ver. 2.0
14   <210> SEQ ID NO 1
15   <211> LENGTH: 27
16   <212> TYPE: DNA
17   <213> ORGANISM: HUMAN
18   <220> FEATURE:
19   <223> OTHER INFORMATION: Upstream primer for PCR amplification.
20   <400> SEQUENCE: 1
21        gcggccgcaa ttgaagttat gtatcct                                   27
22   <210> SEQ ID NO 2
23   <211> LENGTH: 30
24   <212> TYPE: DNA
25   <213> ORGANISM: HUMAN
26   <220> FEATURE:
27   <223> OTHER INFORMATION: Downstream primer for PCR amplification.
28   <400> SEQUENCE: 2
29        tcgaggatct tgtcaggagc gataggctgc                                30
30   <210> SEQ ID NO 3
31   <211> LENGTH: 717
32   <212> TYPE: DNA
33   <213> ORGANISM: HUMAN
34   <220> FEATURE:
35   <223> OTHER INFORMATION: 5F11-scFv
36   <400> SEQUENCE: 3
37        caggtgaaac tgcagcagtc aggacctgaa ctggtgaagc ctggggcttc agtgaagata 60
38        tcctgcaaga cttctggana caaattcact gaatacacca tgcactgggt gaagcagagc 120
39        catggaaaga gccttgagtg gattggaggt attaatccta caatggtgg tactaactac 180
40        aagcagaagt tcaagggcaa ggccacattg actgtagaca gtcctccag cacagcctac 240
41        atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagagatact 300
42        acggtcccgt ttgcttactg ggtccagggg accacggtca ccgtctcctc aggtggaggc 360
43        ggttcaggcg gaggtggctc tggcggtggc ggatcggaca tcgagctcac tcagtctcca 420
44        gcaatcatgt ctgcatctcc aggggagaag gtcaccatga cctgcagtgg cagctcaagt 480
```
W--> 37
W--> 38

All item 10 on Enz summary sheet

```
45         ataagttaca tgcactggta ccagcagaag cctgtcacct cccccaaaag atggatttat 540
46         gacacatcca aactggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 600
47         tcttattctc tcacaatcag cagcatggag gctgtagatg ctgccactta ttactgccat 660
48         cagcggagta gttacccgct cacgttcggt gctgggacac agttggaaat aaaacgg    717
49  <210> SEQ ID NO 4
50  <211> LENGTH: 714
51  <212> TYPE: DNA
52  <213> ORGANISM: HUMAN
53  <220> FEATURE:
54  <223> OTHER INFORMATION: 3G6-scFv
55  <400> SEQUENCE: 4
56         agtattgtga tgacccagac tcccaaattc ctgcttgtat cagcaggaga cagggttacc 60
57         ataacctgca aggccagtca gagtgtgagt aatgatgtgg cttggtacca acagaagcca 120
58         gggcagtctc cgaaactgct gatatactct gcatccaatc gctacactgg agtccctgat 180
59         cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
60         gaagacctgg cagtttattt ctgtcagcag gattatagct cgctcggagg ggggaccaag 300
61         ctggaaataa aaggtggagg cggttcaggc ggaggtggct ctggcggtgg cggatcgcag 360
62         gtgcaggtga aggagtcagg acctggcctg gtggcgccct cacagagcct gtccatcact 420
63         tgcactgtct ctgggttttc attaaccaat tatggtgtac actgggttcg ccagcctcca 480
64         ggaaagggtc tggagtggct gggagtaata tgggctggtg gaagcacaaa ttataattcg 540
65         gctcttatgt ccagactgag catcagcaag gacaactcca agagccaagt tttcttaaaa 600
66         atgaacagtc tgcaaactga tgacacagcc atgtactact gtgccagtcg gggggggtaac 660
67         tacggctatg ctttggacta ctggggtcaa ggaacctcag tcaccgtctc ctca       714
```

Line	?	Error/Warning	Original Text
37	W	"N" or "Xaa" used: Feature required	caggtgaaac tgcagcagtc aggacctgaa ctggtgna
38	W	"N" or "Xaa" used: Feature required	tcctgcaaga cttctggana caaattcact gaatacac